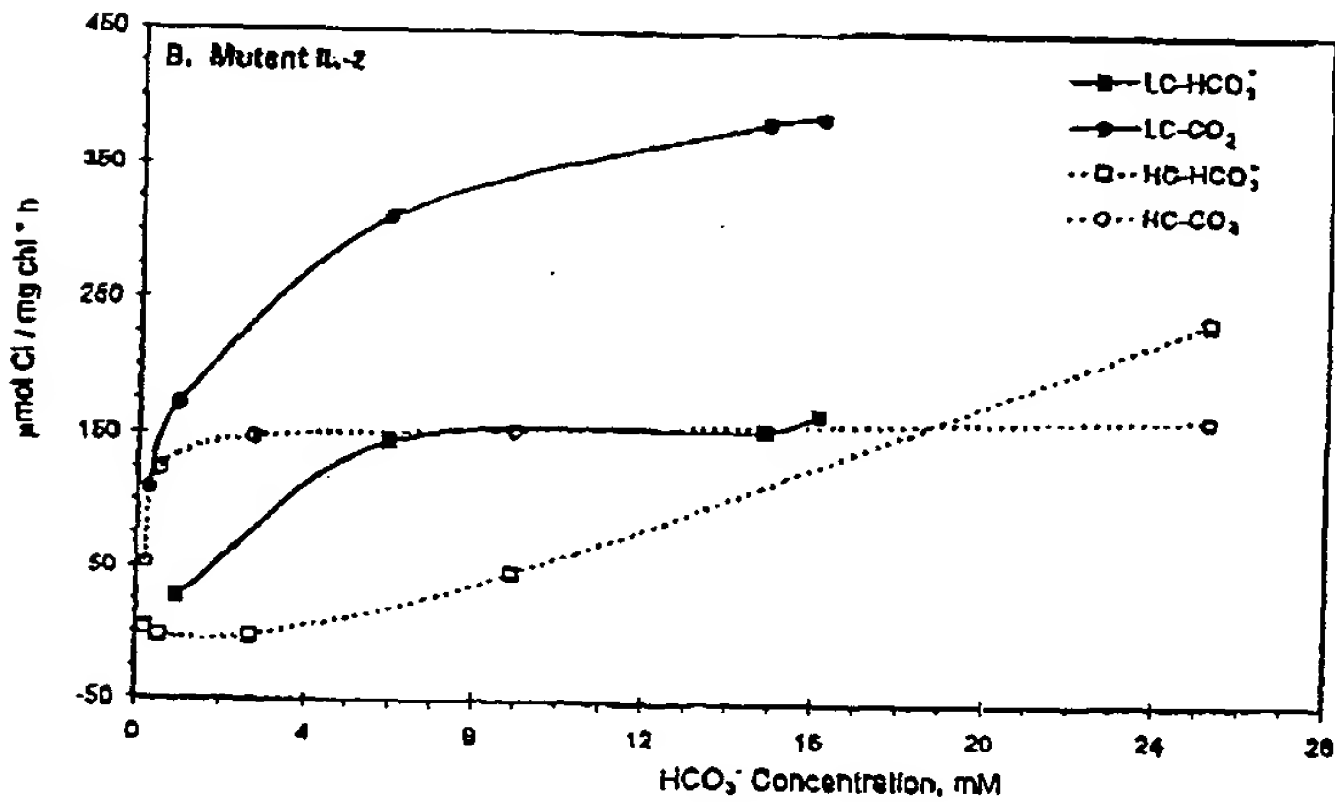
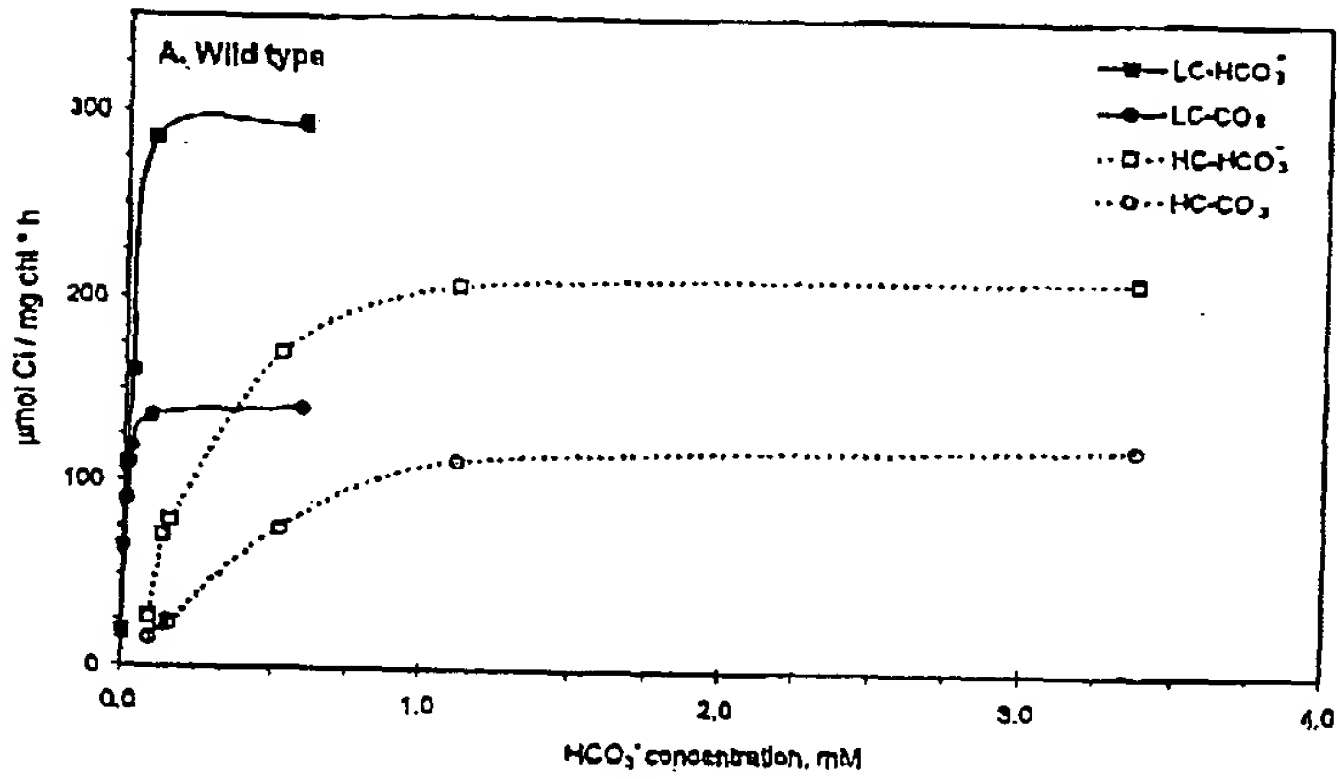
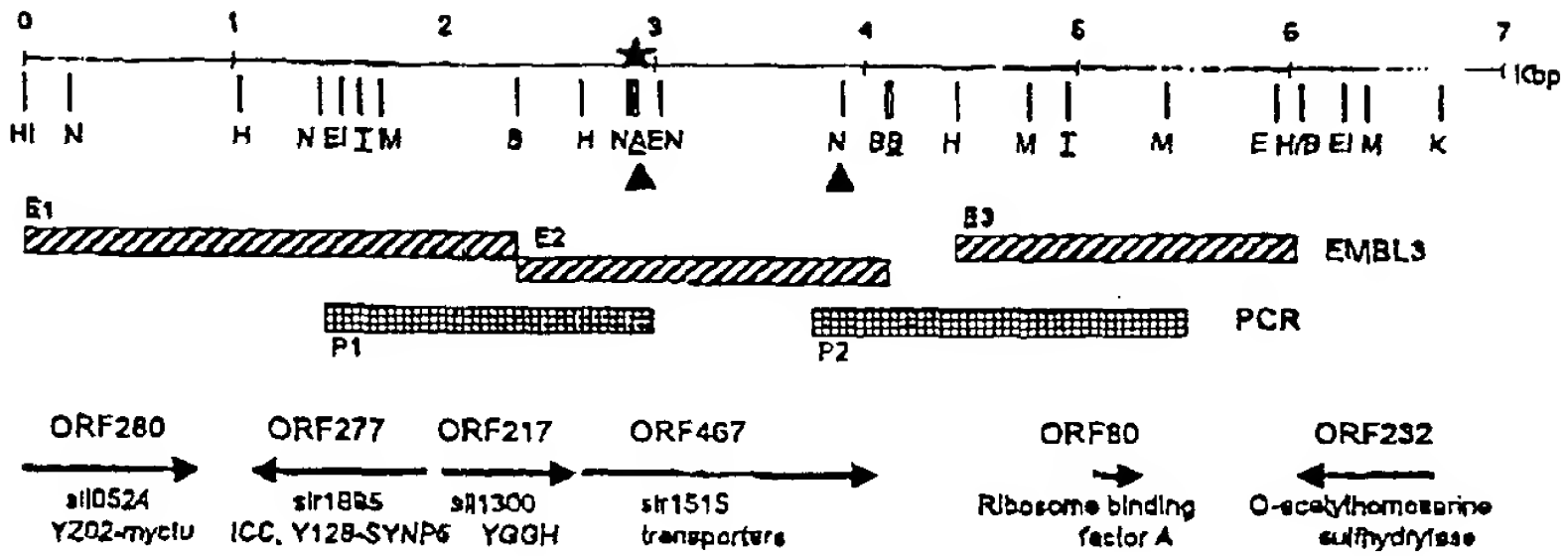


Fig. 1



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[illegible]

[illegible]

ICTB : 943 AACTTCCGGATCAATGTCTGGCTGGCGGTGCTGCAGATGATTCAAGATCGGCCTTGGCTG 1002  
 SLR : 955 AATTTCGCATCAATGTTTGGGAAGGGGTAAAAGCCATGATCCGAGCCCCGCCCTATCATT 1014

ICTB : 1003 GGCATCGGCCCCGGCAATACCGCCTTTAACCTGGTTTATCCCCTCTATCAACAGGCGCGC 1062  
 SLR : 1015 GGCATTGGCCCAGGTAACGAAGCCTTTAACCAAATTTATCCTTACTATATGCGGCCCGCGC 1074

ICTB : 1063 TTTACGGCGTTGAGCGCCTACTCCGTCCCCTGGAAGTCGCGGTTGAGGGCGGACTACTG 1122  
 SLR : 1075 TTCACGCCCTGAGTGCCTATTCCATTTACCTAGAAATTTTGGTGGAAACGGGTGTAGTT 1134

ICTB : 1123 GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGGCGGTGACGGCGGTGCGGCAGG 1180  
 SLR : 1135 GGTTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCTAGGCAAAGGC-GTAGAACTGG 1192

ICTB : 1181 TGAGCCGACTGCGGCGCGATCGCAATCCCC--AAGCCTTTTGGTTGATGGCTAGCTTGGC 1238  
 SLR : 1193 TTAAACG-CTGTGCG-CAAACCCTCGCCCCGGAAGGCATCTGGATTATGGGGGCTTTAGC 1250

ICTB : 1239 CGGTTTGGCAGGAATGCTGGGTACGGTCTGTTTGATACCGTGCTCTATCGACCGGAAGC 1298  
 SLR : 1251 GGCGATCATCGGTTTGTGGTCCACGGCATGGTAGATACAGTCTGGTACCGTCCCCCGGT 1310

ICTB : 1299 CAGTACGCTCTGGTGGCTCTGTATTGG--AGCGATCGCGAGTTTCTGG--CAGC-CCCAA 1353  
 SLR : 1311 GAGCACTTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTGGGCCAGCGCCCAG 1368

ICTB : 1354 CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTTCAGACGAA 1395  
 SLR : 1369 GCCCGTTTGGAGGCCAGTAAAGAA--GAAAATGAGGACAAA 1407

FIGURE 3

ICTB : 1 MTWQTLTFAHYQPQWGHSSFLHRLFGSLRAWRASSQLLVWSEALGGFLLAVVYGSAPF 60  
+++W++L F + PQ+WG S LHRL G ++W +S L EALG L+A+++ +APF  
SLR : 5 ISIWRSMLFGGFSPQEWGRGSVLHRLVGWQSWIQASVLWPHFEALGTALVAIIFIAAPF 64

ICTB : 61 VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVG 120  
++ LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G  
SLR : 65 TSTTMLGIFMLLCGAFWALLTFADQPGKGLTPIHVLVFAYWCISAIAGFSPVKMAAASG 124

ICTB : 121 LAKLTLYLLVFALAARVLRNPRLSLLFSVVVITS LFVSVYGLNQWIYGVEELATWVDRN 180  
LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D  
SLR : 125 LAKLTANLCLFLAARLLQNKQWLNRLVTVLLVGLLVGSYGLRQQVDGVEQLATWNDPT 184

ICTB : 181 SVADFTSRVYSYLGPNPDLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILT 240  
S +RVYS+LGPNPDLAAYLVPT T S +A+ VWR W PKLL + LCL T  
SLR : 185 STLAQATRVYSFLGNPNLLAAYLVPMGTGLSLVWRRWWPKLLGATMVIVNLLCLFFT 244

ICTB : 241 YSRGGWLGFMVAMIFVWALLGLYWFQPRLPAPWRRWLFVVLGGLVAVLLVAVLGLLEPLRV 300  
SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+  
SLR : 245 QSRGGWLAVLALGATFLALCYFWWLPQLPKFWQRWSLPLAIAVAVILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSSNNFRINWLAVLQMIQDRPWLIGPGNTAFNLVYPLYQQARFTALSA 360  
R +SIF GREDSSNNFRINW V MI+ RP +GIGPGN AFN +YP Y + RFTALSA  
SLR : 305 RAMSIFAGREDSSNNFRINWEGVKAMIRARPIIGIGPGNEAFNQIYPYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLGLTAFWALLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLG 420  
YS+ LE+ VE G++G T WLL VT V V R R+ P+ W+M +LA + G+L  
SLR : 365 YSIYLEILVETGVVGFTCMLWLLAVTLGKGVELVKRCRQTLAPEGIWIMGALAAIIGLLV 424

ICTB : 421 HGLFDTVLYRPEASTLWLLCIGAIASFWQPQPSKQLPPEAEHSDEKM 467  
HG+ DTV YRP STLWWL + +AS W ++ + E+ D+ +  
SLR : 425 HGMVDTVWYRPPVSTLWLLVAIVASQWASAQARLEASKEENEDKPL 471

Fig. 5

Wild type GGGCT-AGCCGCGATCGCGGCCTATTGGGCCC (SEQ ID NO: 6)  
IL-2 ApaI side GGGCT-AG--G-GATCGC-GCCTATTGGGCCC (SEQ ID NO: 7)  
IL-2 BamHI side GGGCTCA-----GATCGC-GCCTATTGGGCCC (SEQ ID NO: 8)  
IctB G L A A I A A Y W A L (SEQ ID NO: 9)

Fig. 6

